

# SEQUENCE LISTING

<110> Saha, K.

<120> Methods and Materials Relating to CD8-Tropic HIV-1

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<150> US 60/258,472

<151> 2000-12-28

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<170> PatentIn version 3.1

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 acagctatag cagtagctga ggggacagat aggggttatag aaatagtgca aagaacttgt 2520  
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 <211> 467  
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 <213> HIV-1

<400> 8

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Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr  
 35 40 45

Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His  
 50 55 60

Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln  
 65 70 75 80

Glu Val Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn  
 85 90 95

Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln  
 100 105 110

Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn  
 115 120 125

Cys Thr Asn Val Asn Val Thr Asn Leu Lys Asn Glu Thr Asn Thr Asn  
 130 135 140

Ser Ser Ser Gly Gly Glu Lys Met Glu Glu Gly Glu Met Lys Asn Cys  
 145 150 155 160

Ser Phe Asn Val Thr Thr Leu Ile Arg Asn Lys Arg Lys Thr Glu Tyr  
 165 170 175

Ala Leu Phe Tyr Lys Leu Asp Val Met Pro Ile Asp Arg Asp Asn Thr  
180 185 190

Ser Tyr Thr Leu Ile Asn Cys Lys Ser Ser Thr Ile Thr Gln Ala Cys  
195 200 205

Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala  
210 215 220

Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Asn Gly Lys Gly  
225 230 235 240

Pro Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro  
245 250 255

Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Asp  
260 265 270

Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Asn Ile Ile  
275 280 285

Val Gln Leu Asn Val Ser Leu Glu Ile Asn Cys Thr Arg Pro Asn Asn  
290 295 300

Asn Thr Arg Lys Lys Ile Thr Leu Gly Arg Ser Arg Val Leu Tyr Thr  
305 310 315 320

Thr Gly Glu Ile Ile Gly Asp Ile Arg Arg Ala His Cys Asn Leu Ser  
325 330 335

Arg Thr Ser Trp Asn Asn Thr Leu Lys Gln Ile Val Glu Lys Leu Arg  
340 345 350

Glu Ile Lys Gln Phe Lys Asn Lys Thr Ile Val Phe Lys Gln Ser Ser  
355 360 365

Gly Gly Asp Phe Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu  
370 375 380

Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp His Ala  
385 390 395 400

Asn Gly Thr Trp Lys Asn Thr Glu Gly Ala Asp Asn Asn Ile Thr Leu  
405 410 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly Lys  
420 425 430

Ala Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Arg Cys Leu Ser Asn  
435 440 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Ser Ser Glu Glu Asn  
450 455 460

Gln Thr Glu  
465

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ccaacagacc ccaaccacg agaaataaaa ctggaaaatg tcacagaaaa ctttaacatg 300  
tggaaaaatg acatgggtga gcagatgcat gaggatgtaa tcagtctatg ggatcaaagc 360  
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gcccctaata cactatttaa tgccactgat agggacatag gaatgaaaaa ctgctcttcc 480  
aatgtaacca cagaagtaat aaataagaag aagcaagaac atgcactttt ttataaactt 540  
gatgtggtac aaatggatga taatagtact aataccaact atagattaat aaattgtaat 600  
acctcagtca ttacacaggc gtgtccaaag gtaacctttg agccaattcc catacattat 660  
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acaaataatg ctaaaaccat aatagtacag cttaatgagt ctgtaccaat taattgctca 900  
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gaatttttct actgcgatac atcaagactg tttaatagga cttataatac atcaggtagt 1200  
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gccttcaggc ctggaggagg ggatatgaga gacaattgga gaagtgaatt atacaaatat 1440  
aaagtagtaa gaattgaacc actaggtcta gcacccactg aggcaaagag aagagtggta 1500  
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gctgtgccct ggaactctag ctggagtaat aaatctctaa acgagatttg gggtaacatg 1860  
acctggatgg agtgggaaaa agaaattgac aattacacag aattaatata cagcttaatt 1920  
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agctaccgcc acttgagaga cttaattctta attgcagcga agattgtgga gtttctggga 2340  
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ataagacagg gcttggaag ggctttacta taa 2553

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<212> PRT  
<213> HIV-1

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Gln His Ser Leu Trp Arg Trp Gly Ile Met Leu Leu Gly Met Leu Met  
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Ile Cys Lys Gly Glu Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val  
35 40 45

Trp Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ser  
50 55 60



Tyr Glu Pro Glu Ala His Asn Ile Trp Ala Thr His Ala Cys Val Pro  
65 70 75 80

Thr Asp Pro Asn Pro Arg Glu Ile Lys Leu Glu Asn Val Thr Glu Asn  
85 90 95

Phe Asn Met Trp Lys Asn Asp Met Val Glu Gln Met His Glu Asp Val  
100 105 110

Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro  
115 120 125

Leu Cys Val Thr Leu His Cys Thr Glu Tyr Lys Ala Pro Asn Ala Thr  
130 135 140

Ile Asn Ala Thr Asp Arg Asp Ile Gly Met Lys Asn Cys Ser Phe Asn  
145 150 155 160

Val Thr Thr Glu Val Ile Asn Lys Lys Lys Gln Glu His Ala Leu Phe  
165 170 175

Tyr Lys Leu Asp Val Val Gln Met Asp Asp Asn Ser Thr Asn Thr Asn  
180 185 190

Tyr Arg Leu Ile Asn Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro  
195 200 205

Lys Val Thr Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly  
210 215 220

Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Asn Gly Thr Gly Pro  
225 230 235 240

Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val  
245 250 255

Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Ile  
260 265 270

Ile Ile Arg Ser Glu Asn Leu Thr Asn Asn Ala Lys Thr Ile Ile Val  
275 280 285

Gln Leu Asn Glu Ser Val Pro Ile Asn Cys Ser Arg Pro Tyr Glu Asn  
290 295 300

Lys Arg Arg Arg Thr Pro Ile Gly Leu Gly Gln Tyr Tyr Thr Thr Lys  
305 310 315 320

Leu Lys Gly Tyr Ile Arg Pro Ala His Cys Asn Ile Ser Gly Ala Glu  
325 330 335

Trp Asn Lys Thr Leu Gln Gln Val Ala Lys Lys Leu Gly Asp Leu Phe  
340 345 350

Asn Gln Thr Thr Ile Ile Phe Gln Pro His Ser Gly Gly Asp Pro Glu  
355 360 365

Ile Thr Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp  
370 375 380

Thr Ser Arg Leu Phe Asn Arg Thr Tyr Ser Thr Ser Gly Ser Thr Gly  
385 390 395 400

Val Asn Asn Ser Thr Ile Lys Leu Pro Cys Arg Ile Lys Gln Ile Ile  
405 410 415

Asn Met Trp Gln Gly Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Glu  
420 425 430

Gly Leu Ile Lys Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg  
435 440 445

Asp Gly Gly Asn Asn Thr Arg Gln Asn Glu Ala Phe Arg Pro Gly Gly  
450 455 460

Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val  
465 470 475 480

Val Arg Ile Glu Pro Leu Gly Leu Ala Pro Thr Glu Ala Lys Arg Arg  
485 490 495

Val Val Glu Arg Glu Lys Arg Ala Ile Gly Leu Gly Ala Met Phe Leu  
500 505 510

Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr  
515 520 525

Leu Thr Val Gln Ala Arg Gln Leu Met Ser Gly Ile Val Gln Gln Gln  
530 535 540

Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Thr  
545 550 555 560

Leu Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu  
565 570 575

Ser Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly  
580 585 590

Arg His Ile Cys Thr Thr Ala Val Pro Trp Asn Ser Ser Trp Ser Asn  
595 600 605

Lys Ser Leu Asn Glu Ile Trp Gly Asn Met Thr Trp Met Glu Trp Glu  
610 615 620

Lys Glu Ile Asp Asn Tyr Thr Glu Leu Ile Tyr Ser Leu Ile Glu Glu  
625 630 635 640

Ser Gln Thr Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Lys Leu Asp  
645 650 655

Gln Trp Ala Ser Leu Trp Asn Trp Phe Ser Ile Thr Lys Trp Leu Trp  
660 665 670

Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg  
675 680 685

Ile Val Phe Ala Val Leu Ser Val Val Asn Arg Val Arg Gln Gly Tyr  
690 695 700

Ser Pro Leu Ser Phe Gln Thr Leu Leu Pro Ala Pro Arg Gly Pro Asp  
705 710 715 720

Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly Glu Gln Gly Arg Gly Arg  
725 730 735

Ser Ile Arg Leu Val Thr Gly Phe Ser Ala Leu Ile Trp Asp Asp Leu  
740 745 750

Arg Asn Leu Cys Leu Phe Ser Tyr Arg His Leu Arg Asp Leu Ile Leu  
755 760 765

Ile Ala Ala Lys Ile Val Glu Phe Leu Gly Arg Arg Gly  
770 775 780

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<212> DNA  
<213> HIV-1

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gtacctgtgt ggaaagatgc agaaaccacc ttattttgtg catcagatgc gaaagcatat 180

gatacagaag	tgcataatgt	ctgggccaca	catgcctgtg	tacctacaga	ccccaaccca	240
caagaaataa	atttggaaaa	tgtgacagaa	aattttaaca	tgtggaaaaa	taacatggta	300
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aaggataaga	cacagaaagt	acgttcattt	ttctataaga	tggatatagt	acaaattaac	540
aacaacaaca	gcaacagcaa	cagtagtcag	tatagattaa	taagttgtaa	tacctcaacc	600
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ataatagggg	atataagaca	agcacattgt	aacatcagta	gagcagcatg	gaataacact	1020
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agaatattta	taatgatagt	aggaggctta	ataggattaa	gaatagtttt	tgctgtaatt	2100

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caataa 2586

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<212> PRT  
<213> HIV-1

<400> 12

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Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Asp Ala Glu Thr  
35 40 45

Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His  
50 55 60

Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln  
65 70 75 80

Glu Ile Asn Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn  
85 90 95

Asn Met Val Glu Gln Met His Thr Asp Ile Ile Ser Leu Trp Asp Gln  
100 105 110

Ser Leu Lys Pro Cys Val Gln Leu Thr Pro Leu Cys Val Thr Leu Asp  
115 120 125

Cys Thr Asp Ala Thr Asn Ala Thr Asn Thr Thr Ile Ile Ser Asp Met  
130 135 140

Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn Met Thr Thr Glu Leu Lys  
145 150 155 160

Asp Lys Thr Gln Lys Val Arg Ser Phe Phe Tyr Lys Met Asp Ile Val  
165 170 175

Gln Ile Asn Asn Asp Asn Asn Ser Asn Ser Asn Ser Ser Gln Tyr Arg  
180 185 190

Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val  
195 200 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala  
210 215 220

Ile Leu Lys Cys Lys Asp Lys Glu Phe Asn Gly Thr Gly Pro Cys Arg  
225 230 235 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Lys Pro Val Val Ser  
245 250 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Lys Val Met Ile  
260 265 270

Arg Ser Glu Asn Ile Thr Asp Asn Thr Lys Asn Ile Ile Val Gln Leu  
275 280 285

Thr Glu Pro Val Lys Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg  
290 295 300

Arg Gly Ile Ser Ile Gly Pro Gly Arg Ala Phe Ile Ala Arg Asp Arg  
305 310 315 320

Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Arg Ala Ala  
325 330 335

Trp Asn Asn Thr Leu Gln Lys Val Ala Gln Gln Leu Arg Thr His Phe  
340 345 350

Glu Asn Arg Thr Ile Ile Phe Asn His Ser Ala Gly Gly Asp Pro Glu  
355 360 365

Ile Thr Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Ser  
370 375 380

Thr Thr Gly Leu Phe Asn Ser Thr Trp Ala Ser Asn Ala Ser Thr Gln  
385 390 395 400

Gly Ser Asn Ser Thr Gly Ser Asn Asp Thr Ile Thr Leu Gln Cys Arg  
405 410 415

Ile Arg Gln Ile Ile Arg Met Trp Gln Arg Val Gly Gln Ala Met Tyr  
 420 425 430

Ala Pro Pro Ile Pro Gly Val Ile Arg Cys Asp Ser Asn Ile Thr Gly  
 435 440 445

Leu Ile Leu Thr Arg Asp Gly Gly Asp Asn Asn Ser Thr Asn Glu Thr  
 450 455 460

Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu  
 465 470 475 480

Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr  
 485 490 495

Arg Ala Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala Ile Ala Gly  
 500 505 510

Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met  
 515 520 525

Gly Ala Ala Ser Leu Thr Leu Thr Val Gln Thr Arg Gln Leu Leu Ser  
 530 535 540

Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln  
 545 550 555 560

Gln His Leu Leu Lys Thr Leu Val Trp Gly Ile Lys Gln Leu Gln Ala  
 565 570 575

Arg Val Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly  
 580 585 590

Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Thr Val Pro Trp  
 595 600 605

Asn Ser Ser Trp Ser Asn Lys Ser Tyr Ser Glu Ile Trp Asp Asn Met  
 610 615 620

Thr Trp Leu Gln Glu Trp Lys Glu Ile Ser Asn Tyr Thr Gln Ile Ile  
 625 630 635 640

Tyr Asp Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln  
 645 650 655

Asp Leu Leu Ala Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp  
 660 665 670

Ile Ser Lys Trp Leu Trp Tyr Ile Arg Ile Phe Ile Met Ile Val Gly  
675 680 685

Gly Leu Ile Gly Leu Arg Ile Val Phe Ala Val Ile Ser Val Ile Asn  
690 695 700

Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Leu Ala Pro  
705 710 715 720

Asn Pro Gly Gly Leu Asp Arg Pro Gly Arg Ile Glu Glu Glu Gly Gly  
725 730 735

Glu Gln Asp Arg Ser Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala  
740 745 750

Leu Ala Trp Glu Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg  
755 760 765

Leu Arg Asp Phe Ile Leu Ile Ala Ala Arg Thr Val Glu Leu Leu Gly  
770 775 780

His Ser Ser Leu Lys Gly Leu Arg Leu Gly Trp Glu Gly Leu Lys Tyr  
785 790 795 800

Leu Gly Asn Leu Leu Leu Tyr Trp Gly Gln Glu Leu Lys Ile Ser Ala  
805 810 815

Ile Ser Leu Phe Asp Thr Ile Ala Ile Val Ile Ala Gly Trp Thr Asp  
820 825 830

Arg Val Ile Glu Ile Gly Gln Arg Ile Gly Arg Ala Ile Leu Asn Ile  
835 840 845

Pro Arg Arg Ile Arg Gln Gly Ala Glu Arg Ala Leu Gln  
850 855 860

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<211> 2607  
<212> DNA  
<213> HIV-1

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gggggtacctg tgtggaaaga agcaaacc actctatttt gtgcatcaga tgctaaagca 180  
tatgatacag aggcacataa tgtttgggcc acacatgcct gtgtaccac agaccccaac 240



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aaattaaccc	cactctgtgt	tacttttaaat	tgcactgatg	taaggaatgg	tactattgtg	420
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<400> 14

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Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Asn Thr  
 35 40 45

Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Ala His  
 50 55 60

Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln  
 65 70 75 80

Glu Ile Val Leu Ala Asn Val Thr Glu Asp Phe Asn Met Trp Lys Asn  
 85 90 95

Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln  
 100 105 110

Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn  
 115 120 125

Cys Thr Asp Val Arg Asn Gly Thr Ile Val Arg Asn Ser Thr Ile Arg  
 130 135 140

Val Glu Glu Gly Met Lys Glu Glu Ile Lys Asn Cys Ser Phe Asn Val  
 145 150 155 160

Thr Thr Ser Met Gly Asp Lys Leu Gln Lys Glu Asp Ala Phe Phe Tyr  
165 170 175

Lys Ser Asp Val Val Gln Met Gly Asp Asn Asn Asn Thr Asn Thr Ser  
180 185 190

Asn Asn Asn Ile Thr Tyr Thr Ser Tyr Arg Leu Arg Ser Cys Asn Thr  
195 200 205

Ser Val Ile Thr Gln Ala Cys Pro Lys Ile Asn Phe Glu Pro Ile Pro  
210 215 220

Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn  
225 230 235 240

Arg Thr Phe Glu Gly Lys Gly Pro Cys Lys Asn Val Ser Thr Val Gln  
245 250 255

Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn  
260 265 270

Gly Ser Leu Ala Glu Lys Asp Ile Val Ile Arg Ser Ala Asn Phe Ser  
275 280 285

Asp Asn Ala Lys Ala Ile Ile Val Gln Leu Asn Glu Thr Val Gln Ile  
290 295 300

Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Arg Ile Thr Met Gly  
305 310 315 320

Pro Gly Ala Val Tyr Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile Arg  
325 330 335

Arg Ala His Cys Asn Ile Ser Lys Glu Asp Trp Thr Asn Thr Leu Lys  
340 345 350

Gln Ile Ala Lys Lys Leu Arg Glu Gln Phe Gly Asp Asn Lys Thr Ile  
355 360 365

Ala Phe Lys Pro Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser  
370 375 380

Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Thr Thr Lys Leu Phe  
385 390 395 400

Asn Ser Thr Trp Phe Gly Asn Ser Thr Arg Asn Asn Thr Glu Gly Ser  
405 410 415

Ser Asn Asn Gly Asn Ile Thr Leu Gln Cys Arg Ile Lys Gln Ile Ile  
420 425 430

Asn Met Trp Gln Gly Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Arg  
435 440 445

Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg  
450 455 460

Asp Gly Gly Asn Thr Asn Asp Thr Asn Asn Thr Glu Ile Phe Arg Pro  
465 470 475 480

Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr  
485 490 495

Lys Val Val Lys Ile Glu Pro Leu Gly Ile Ala Pro Thr Lys Ala Lys  
500 505 510

Arg Arg Val Val Gln Arg Glu Lys Arg Ala Met Gly Ile Gly Ala Leu  
515 520 525

Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser  
530 535 540

Met Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln  
545 550 555 560

Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln His His Leu Leu  
565 570 575

Gln Thr Leu Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala  
580 585 590

Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys  
595 600 605

Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp  
610 615 620

Ser Asn Lys Ser Leu Asp Lys Ile Trp Asn Asn Met Thr Trp Met Gln  
625 630 635 640

Trp Glu Arg Glu Ile Asp Asn Tyr Thr Ser Leu Ile Tyr Thr Leu Ile  
645 650 655

Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Leu Glu Leu Leu Glu  
660 665 670

Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Thr Lys Trp  
675 680 685

Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly  
690 695 700

Leu Arg Ile Val Phe Val Ile Leu Ser Ile Val Asn Arg Val Arg Gln  
705 710 715 720

Gly Tyr Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro Ala Gln Arg Gly  
725 730 735

Pro Asp Arg Pro Glu Gly Ile Glu Glu Gly Gly Gly Arg Gly Arg  
740 745 750

Asp Thr Ser Gly Pro Leu Val Asp Gly Phe Leu Ala Ile Ile Trp Val  
755 760 765

Asp Leu Arg Ser Leu Phe Leu Phe Ser Tyr His Arg Leu Arg Asp Leu  
770 775 780

Leu Leu Ile Ala Thr Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp  
785 790 795 800

Glu Ile Leu Lys Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ile Gln Glu  
805 810 815

Leu Lys Asn Ser Ala Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val  
820 825 830

Ala Glu Gly Thr Asp Arg Ile Ile Glu Val Ala Arg Arg Thr Phe Arg  
835 840 845

Ala Ile Leu His Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala  
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Leu Leu  
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<400> 16

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Thr Met Leu Leu Gly Leu Leu Met Ile Cys Ser Ala Ala Asp Gln Leu  
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Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Thr Thr Thr  
35 40 45

Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Lys Glu Val His  
50 55 60

Asn Val Trp Ala Thr Met Ala Cys Val Pro Thr Phe Pro Asn Pro Gln  
65 70 75 80

Ile Val Glu Asn Phe Asn Met Leu Lys Asn Asn Met Val Glu Gln Asp  
85 90 95

His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Thr  
100 105 110

Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr Asp Asp Leu Arg  
115 120 125

Asn Ala Asn Asn Thr Thr Thr Asn Thr Asn Ser Asn Trp Glu Lys Pro  
130 135 140

Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Lys Ile Thr Ser Ser  
145 150 155 160

Ile Arg Asp Lys Val Gln Lys Gln Tyr Ala Leu Phe Tyr Ser Leu Asp  
165 170 175

Val Val Pro Ile Lys Asn Asn Asn Asn Ile Ser Asn Lys Ile Arg Tyr  
180 185 190

Arg Leu Arg Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys  
195 200 205

Val Thr Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe  
210 215 220

Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Asn Gly Thr Gly Pro Cys  
225 230 235 240

Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Asn Val Val  
245 250 255

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val  
260 265 270

Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln  
275 280 285

Leu Lys Asp Pro Val Glu Ile Asn Cys Thr Arg Pro Asn Arg Asn Ala  
290 295 300

Trp Lys Gly Ile Pro Ile Gly Val Pro Gly Arg Lys Phe Tyr Ala Arg  
305 310 315 320

Arg Asn Ile Thr Gly Asp Ile Arg Gln Ala Tyr Cys Asn Leu Ser Ile  
325 330 335

Ala Lys Trp Thr Asn Thr Leu Lys Gln Ile Val Glu Lys Leu Arg Leu  
340 345 350

His Phe Lys Asn Lys Thr Ile Val Phe Lys Ser Ser Ser Gly Gly Asp  
355 360 365

Pro Glu Ile Ile Leu His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr  
370 375 380

Cys Asn Ser Thr Lys Leu Phe Asn Ser Thr Trp Phe Ser Thr Thr Glu  
385 390 395 400

Gly Leu Asn Asn Thr Gly Asn Glu Asp Pro Ile Val Leu Pro Cys Arg  
405 410 415



Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr  
420 425 430

Ala Pro Pro Ile Ala Asp Leu Ile Arg Cys Ser Ser Asn Ile Thr Gly  
435 440 445

Leu Leu Leu Thr Arg Asp Gly Gly Val Asp Glu Asn Ser Asn Thr Thr  
450 455 460

Glu Thr Phe Arg Pro Gly Gly Gly Asn Met Arg Asp Asn Trp Arg Ser  
465 470 475 480

Glu Leu Tyr Lys Tyr Lys Ala Val Lys Ile Glu Pro Leu Gly Val Ala  
485 490 495

Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val  
500 505 510

Gly Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr  
515 520 525

Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Gln Leu Leu  
530 535 540

Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala  
545 550 555 560

Gln Gln His Leu Leu Gln Thr Leu Val Trp Gly Ile Lys Gln Leu Gln  
565 570 575

Ala Arg Val Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu  
580 585 590

Gly Phe Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro  
595 600 605

Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Asp Arg Ile Trp Asn Asn  
610 615 620

Met Thr Trp Met Glu Trp Glu Arg Glu Ile Asp Asn Tyr Thr Gly Leu  
625 630 635 640

Ile Tyr Asn Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu  
645 650 655

Gln Glu Leu Leu Ala Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe  
660 665 670

Asp Ile Thr Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val  
675 680 685

Gly Gly Leu Ile Gly Leu Arg Ile Val Phe Thr Val Leu Ser Ile Val  
690 695 700

Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His His  
705 710 715 720

Pro Ala Gln Arg Glu Pro Asp Arg Pro Glu Gly Ile Glu Gly Glu Gly  
725 730 735

Gly Glu Arg Asp Arg Asp Arg Ser Gly Pro Leu Val Asp Gly Phe Leu  
740 745 750

Ala Ile Ile Trp Val Asp Leu Arg Ser Leu Cys Ile Phe Leu Tyr His  
755 760 765

Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu Leu  
770 775 780

Gly Arg Arg Gly Trp Glu Val Leu Lys Tyr Trp Trp Asn Leu Leu Gln  
785 790 795 800

Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Ile Asn Leu Leu Asn Ala  
805 810 815

Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Ile Leu  
820 825 830

Gln Arg Ala Phe Arg Ala Ile Leu His Ile Pro Thr Arg Ile Arg Gln  
835 840 845

Gly Leu Glu Arg Ala Leu Leu  
850 855

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gatacagagg cacataatgt ttgggccaca catgcctgtg tacccacaga cccaaccca 240

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gaacagatgc	atgaggatat	aatcagtcta	tgggatcaaa	gcctaaagcc	atgtgtaaaa	360
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Asp Val Val Pro Ile Lys Asp Ala Lys Asp Ser Asn Ser Tyr Arg Leu  
180 185 190

Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val Ser  
195 200 205

Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile  
210 215 220

Leu Lys Cys Asn Asn Lys Thr Phe Ser Gly Lys Gly Gln Cys Lys Asn  
225 230 235 240

Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Ala Ser Thr  
245 250 255

Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Lys Asp Ile Ile Ile Arg  
260 265 270

Ser Asp Asn Phe Ser Asp Asn Ala Lys Ile Ile Ile Val Gln Leu Lys  
275 280 285

Glu Pro Val Glu Ile Asn Cys Thr Arg Pro Gly Asn Asn Thr Arg Lys  
290 295 300

Ser Ile His Ile Gly Pro Gly Arg Ala Trp Tyr Ala Thr Gly Asp Ile  
305 310 315 320

Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Ser Val Lys Trp  
325 330 335

Asn Asn Thr Leu Arg Gln Ile Ala Lys Lys Leu Gly Glu Gln Phe Gln  
340 345 350

Asp Lys Asn Ile Thr Phe Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile  
355 360 365

Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ala  
370 375 380

Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Gly Thr Trp Asn Asn Ser  
385 390 395 400

Thr Trp Asn Glu Thr Asp Thr Thr Thr Ile Thr Leu Pro Cys Arg Ile  
405 410 415

Lys Gln Ile Val Asn Met Trp Gln Thr Val Gly Arg Ala Met Tyr Ala  
420 425 430

Pro Pro Ile Arg Gly Glu Ile Ser Cys Ser Ser Asn Ile Thr Gly Leu  
435 440 445

Leu Leu Thr Arg Asp Gly Gly Asn Ile Asn Glu Thr Asn Gly Thr Glu  
450 455 460

Ile Phe Arg Pro Ala Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu  
465 470 475 480

Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Ile Ala Pro  
485 490 495

Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val Gly  
500 505 510

Val Gly Ala Met Phe Leu Gly Phe Leu Ser Ala Ala Gly Ser Thr Met  
515 520 525

Gly Ala Ala Ser Val Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser  
530 535 540

Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln  
545 550 555 560

Gln His Leu Leu Gln Thr Leu Val Trp Gly Ile Lys Gln Leu Gln Ala  
565 570 575

Arg Val Leu Ala Val Glu Arg Tyr Leu Gly Asp Gln Gln Leu Leu Gly  
580 585 590

Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Thr Val Pro Trp  
595 600 605

Asn Thr Ser Trp Ser Asn Lys Ser Leu Lys Tyr Ile Trp Asp Asn Met  
610 615 620

Thr Trp Met Gln Trp Asp Lys Glu Ile Ser Asn Tyr Thr Gly Leu Ile  
625 630 635 640

Tyr Thr Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys  
645 650 655

Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asp  
660 665 670

Ile Thr Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Ile Ile Val Gly  
675 680 685

Gly Leu Ile Gly Leu Arg Ile Val Phe Thr Val Leu Ser Ile Val Asn  
690 695 700

Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro  
705 710 715 720

Thr Gln Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly  
725 730 735

Glu Arg Asp Arg Asp Arg Ser Arg Thr Ser Val Asp Gly Phe Leu Ala  
740 745 750

Leu Ile Trp Val Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg  
755 760 765

Leu Arg Asp Leu Leu Leu Ile Leu Ala Arg Ile Val Glu Leu Leu Gly  
770 775 780

Arg Arg Gly Trp Glu Thr Leu Arg Tyr Trp Trp Asn Leu Leu Gln Tyr  
785 790 795 800

Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn Ser Ile  
805 810 815

Ala Ile Val Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val Val Gln  
820 825 830

Arg Val Cys Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg Gln Gly  
835 840 845

Leu Glu Arg Ala Leu Leu  
850

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<211> 2589  
<212> DNA  
<213> HIV-1

<400> 19  
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gtacccgtgt ggaaagaagc aaccaccact ctattctgtg catctgatgc taaagcatat 180  
gatacagaga aacataatgt ttgggccaca catgcctgtg tacctacaga cccaaccca 240  
caagaagtag tattggaaaa tgtgacagaa aattttaaca tgtggaaaaa taacatggta 300  
gaacagatgc atgaggatat aatcagttta tgggatcaaa gtctaaagcc atgtgtaaaa 360

ctaaccacac	tctgtgtcac	tttaaactgt	aggaacgtta	ctattaccaa	tactactacc	420
aatagtagtg	gctggaaact	aatggaggaa	ggagaaataa	aaaactgctc	tttcaaaatc	480
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gtaccactag	gtaataatag	tgcaataggt	aataataatg	ccagatatag	gttgataagt	600
tgtaacacct	caaccattac	acaggcctgt	ccaaagggtat	cctttgagcc	aattcccata	660
cattattgtg	ccccggctgg	ttttgctgatt	ctaaaatgta	gagataagaa	gttcaatgga	720
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tcaactcaac	tactgtttaa	tggcagctcta	gcagaagaag	atatagtaat	tagatctgcc	840
aattttctcag	acaatgctaa	aatcataata	gtacagctga	ataaaactgt	agtaattaat	900
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gaatggtata	acacttttaa	gcaggtagtt	acaaaattag	gagaacattt	taagaataaa	1080
acaatagcct	ttaataaatc	ctcaggaggg	gaccacagaaa	ttgtaaagca	cactttttaat	1140
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aagaatgaac	aagacttatt	agcattggat	aaatgggcaa	gtttgtggga	ttgggttagc	2040
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ttaagaataa	tttttactgt	actttctata	gtgaatagag	ttaggcaggg	atactcacca	2160
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gaaggagggtg	gagagaaaga	cagagacaga	tccgggctat	tagtgaacgg	attccttgca	2280



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tattgggtgga atctcctgca gtattggagt caggaactaa agaatagtgc tgttagcttg 2460  
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<210> 20  
<211> 862  
<212> PRT  
<213> HIV-1

<400> 20

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Gly Ile Met Leu Leu Gly Leu Leu Met Ile Cys Ser Ala Ala Glu Gln  
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Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr  
35 40 45

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Lys  
50 55 60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro  
65 70 75 80

Gln Glu Val Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys  
85 90 95

Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp  
100 105 110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu  
115 120 125

Asn Cys Arg Asn Val Thr Ile Thr Asn Thr Thr Thr Asn Ser Ser Gly  
130 135 140

Trp Lys Leu Met Glu Glu Gly Glu Ile Lys Asn Cys Ser Phe Lys Ile  
145 150 155 160

Thr Thr Ile Leu Arg His Lys Met Gln Glu Glu His Ala Leu Phe Tyr  
165 170 175

Lys Ser Asp Val Val Pro Leu Gly Asn Asn Ser Ala Ile Gly Asn Asn  
180 185 190

Asn Ala Arg Tyr Arg Leu Ile Ser Cys Asn Thr Ser Thr Ile Thr Gln  
195 200 205

Ala Cys Pro Lys Val Thr Phe Glu Pro Ile Pro Ile His Tyr Cys Ala  
210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Arg Asp Lys Lys Phe Asn Gly  
225 230 235 240

Thr Gly Pro Cys Lys Asp Val Ser Thr Val Gln Cys Thr His Gly Ile  
245 250 255

Lys Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu  
260 265 270

Glu Asp Ile Val Ile Arg Ser Ala Asn Phe Ser Asp Asn Ala Lys Ile  
275 280 285

Ile Ile Val Gln Leu Asn Lys Thr Val Val Ile Asn Cys Thr Arg Pro  
290 295 300

Asn Asn Asn Thr Arg Lys Gly Ile Asn Ile Gly Pro Gly Arg Thr Val  
305 310 315 320

Tyr Ala Thr Gly Lys Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn  
325 330 335

Ile Ser Lys Gly Glu Trp Tyr Asn Thr Leu Lys Gln Val Val Thr Lys  
340 345 350

Leu Gly Glu His Phe Lys Asn Lys Thr Ile Ala Phe Asn Lys Ser Ser  
355 360 365

Gly Gly Asp Pro Glu Ile Val Lys His Thr Phe Asn Cys Gly Gly Glu  
370 375 380

Phe Phe Tyr Cys Asp Ser Thr Lys Leu Phe Thr Ser Thr Trp Asn Tyr  
385 390 395 400

Thr Asn Gly Thr Trp Asn Ser Thr Asn Trp Asn Asp Thr Glu Met Leu  
405 410 415

Asn Lys Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Val Asn Met  
420 425 430

Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Leu  
435 440 445

Ile Thr Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly  
450 455 460

Gly Ser Asn Thr Asn Thr Thr Glu Val Phe Arg Pro Gly Gly Gly Asn  
465 470 475 480

Met Lys Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys  
485 490 495

Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val  
500 505 510

Gln Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe  
515 520 525

Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Leu Thr Leu Thr  
530 535 540

Val Gln Thr Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn  
545 550 555 560

Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Thr Leu Val  
565 570 575

Trp Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Val Glu Arg Tyr  
580 585 590

Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu  
595 600 605

Ile Cys Thr Thr Thr Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser  
610 615 620

Leu Asp Asp Ile Trp Asn Asn Met Thr Trp Met Glu Trp Glu Arg Glu  
625 630 635 640

Ile Asp Asn Tyr Thr Asn Val Ile Tyr Asn Leu Ile Glu Glu Ser Gln  
645 650 655

Asn Gln Gln Glu Lys Asn Glu Gln Asp Leu Leu Ala Leu Asp Lys Trp  
660 665 670

Ala Ser Leu Trp Asp Trp Phe Ser Ile Ser Asn Trp Leu Trp Tyr Ile  
675 680 685

Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg Ile Ile  
690 695 700

Phe Thr Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro  
705 710 715 720

Leu Ser Phe Gln Thr Arg Phe Pro Ala Pro Arg Gly Pro Asp Arg Pro  
725 730 735

Glu Gly Ile Glu Glu Gly Gly Gly Glu Lys Asp Arg Asp Arg Ser Gly  
740 745 750

Leu Leu Val Asn Gly Phe Phe Ala Leu Ile Trp Val Asp Leu Arg Ser  
755 760 765

Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Ala  
770 775 780

Ala Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ile Leu Lys  
785 790 795 800

Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser  
805 810 815

Ala Val Ser Leu Leu Asn Val Thr Ala Ile Ala Val Ala Glu Gly Thr  
820 825 830

Asp Arg Ile Leu Glu Val Leu Gln Arg Ala Tyr Arg Ala Ile Ile His  
835 840 845

Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Leu  
850 855 860

<210> 21

<211> 2598

<212> DNA

<213> HIV-1

<400> 21

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gtgtggagag acgcagagac caccttattt tgtgcatcag atgctaaagc atatgataca 180

gaagtacata atgtttgggc tacacatgcc tgtgtaccca cagaccctaa cccacaagaa 240

atacctttgg aaaatgtaac agaaaatttt aatatgtgga aaaataacat ggtagagcag 300



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gccctcaa atctgtggaa tcttctgtca tactggggcc aggaactaaa gaatagtgt 2460  
attaatctgc ttgatacaac agcaatagca gtagctaatt ggacagacag agttatagaa 2520  
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gaaagggctt tgcaataa 2598

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<211> 864  
<212> PRT  
<213> HIV-1

<400> 22

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Ile Ile Phe Trp Ile Met Val Ile Cys Asn Ala Glu Asn Leu Trp Val  
20 25 30

Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Asp Ala Glu Thr Thr Leu  
35 40 45

Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His Asn Val  
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Phe Pro Asn Pro Gln Glu Ile  
65 70 75 80

Pro Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met  
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Asp Trp Asp Gln Ser Leu  
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr  
115 120 125

His Asn Phe Asn Asn Phe Asn Ser Ser Asn Asn Ser Thr Pro Ile Asn  
130 135 140

Asn Thr Ile Tyr Asn Gly Met Gln Gly Glu Ile Lys Asn Cys Ser Phe  
145 150 155 160

Asn Thr Thr Thr Glu Leu Arg Gly Lys Thr Lys Lys Gln Tyr Ala Leu

165

170

175

Phe Asn Lys Leu Asp Val Val Gln Ile Asn Asp Lys Asn Asn Ser His  
180 185 190

Ser Asn Asn Arg Arg Tyr Met Leu Ile His Cys Asn Thr Ser Val Ile  
195 200 205

Thr Gln Ala Cys Pro Lys Val Thr Phe Glu Pro Ile Pro Ile Tyr Tyr  
210 215 220

Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Lys Asp Gln Glu Phe  
225 230 235 240

Asn Gly Ser Gly Pro Cys Asn Asn Val Ser Thr Val Gln Cys Thr His  
245 250 255

Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu  
260 265 270

Ala Glu Arg Lys Ile Met Ile Arg Ser Glu Asn Ile Thr Asn Asn Ala  
275 280 285

Lys Thr Ile Ile Val Gln Phe Thr Glu Pro Val Glu Ile Asn Cys Thr  
290 295 300

Arg Pro Asn Asn Asn Thr Arg Lys Arg Val Gly Val Gly Pro Gly Arg  
305 310 315 320

Ala Val Tyr Val Thr Asn Ala Ile Ile Gly Asp Ile Arg Gln Ala Tyr  
325 330 335

His Asn Val Ser Arg Ala Lys Trp Asn Asp Thr Leu Lys Lys Val Val  
340 345 350

Thr Gln Leu Arg Lys His Phe Asn Thr Thr Ile Val Phe Thr Lys Pro  
355 360 365

Ser Gly Gly Asp Val Glu Ile Thr Thr His Ser Phe Asn Cys Gly Gly  
370 375 380

Glu Phe Phe Tyr Cys Asn Thr Ser Gln Leu Phe Asn Ser Thr Trp Ile  
385 390 395 400

Ile Asn Gly Thr Asn His Thr Gly Pro Tyr Asp Thr Asp Thr Ile Thr  
405 410 415

Leu Arg Cys Arg Ile Lys Gln Ile Val Lys Thr Trp Gln Arg Val Gly  
420 425 430

Gln Ala Met Tyr Ala Pro Pro Ile Pro Gly Val Ile Arg Cys Asp Ser  
435 440 445

Asn Ile Thr Gly Ile Leu Leu Thr Arg Asp Gly Gly Lys Ile Asn Ser  
450 455 460

Thr Asn Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp  
465 470 475 480

Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly  
485 490 495

Val Ala Pro Thr His Ala Lys Arg Arg Val Val Glu Arg Glu Lys Arg  
500 505 510

Ala Val Gly Val Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala  
515 520 525

Gly Ser Thr Met Gly Ala Ala Ala Ile Thr Leu Thr Val Gln Ala Arg  
530 535 540

Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala  
545 550 555 560

Ile Glu Ala Gln Gln His Leu Leu Lys Thr Leu Val Trp Gly Ile Lys  
565 570 575

Gln Leu Gln Ala Arg Val Leu Ala Leu Glu Arg Tyr Leu Arg Asp Gln  
580 585 590

Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr  
595 600 605

Asn Val Pro Trp Asn Ser Ser Trp Ser Asn Lys Thr Phe Asn Asp Ile  
610 615 620

Trp Asn Met Thr Trp Leu Gln Trp Asp Lys Glu Ile Asn Asn Tyr Thr  
625 630 635 640

Asn Thr Ile Tyr Arg Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys  
645 650 655

Asn Glu Gln Asp Leu Leu Ala Leu Asp Lys Trp Ala Ser Leu Trp Ser  
660 665 670



Trp Phe Asp Leu Ser Asn Trp Leu Trp Tyr Ile Arg Ile Phe Ile Met  
675 680 685

Val Val Gly Gly Leu Ile Ala Leu Arg Ile Val Phe Ala Val Leu Ala  
690 695 700

Ile Ile Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr  
705 710 715 720

Leu Thr His His Gln Arg Glu Pro Asp Arg Pro Glu Gly Ile Glu Glu  
725 730 735

Gly Gly Gly Glu Gln Asp Arg Asp Arg Ser Val Arg Leu Val Asn Gly  
740 745 750

Phe Leu Ala Leu Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser  
755 760 765

Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Ala Ala Arg Thr Val Glu  
770 775 780

Leu Leu Gly His Ser Ser Leu Lys Gly Leu Arg Leu Gly Trp Gly Ala  
785 790 795 800

Leu Lys Tyr Leu Trp Asn Leu Leu Ser Tyr Trp Gly Gln Glu Leu Lys  
805 810 815

Asn Ser Ala Ile Asn Leu Leu Asp Thr Thr Ala Ile Ala Val Ala Asn  
820 825 830

Trp Thr Asp Arg Val Ile Glu Ile Gly Gln Arg Phe Gly Arg Ala Ile  
835 840 845

Leu Asn Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Gln  
850 855 860

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<212> DNA  
<213> Primer

<400> 23  
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24

<210> 24  
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<400> 24  
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24

<210> 25  
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<213> Primer

<400> 25  
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25

<210> 26  
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<400> 26  
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26

<210> 27  
<211> 7  
<212> PRT  
<213> Peptide

<400> 27  
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